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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-q9y4x1.res made by jdelaval on Sun 2 Sep 101 10:48:09-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File: q9y4x1.pap

100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
S -
E 5-
O -
U -
N -
E -
C -
E -
S 0-
SCORE 0 1 1 2 2 3 3 4 4 5
STDV

PARAMETERS

Similarity matrix Unitary K-tuple 2
Translation Frame 6
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 5 Median 0 Standard Deviation 0.00

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 527
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Int. Opt.	Sig. Frame
1. q9y4x1	UDP GLUCURONOSYLTRANSFERASE (527	5	89	0.00 1

1. US-09-784-340-1 (1-2759)
q9y4x1 UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4x1 check: 7657 from: 1 to: 527

ID Q9Y4X1 PRELIMINARY; PRT; 527 AA.
AC Q9Y4X1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OLEFACTORY;
RX MEDLINE=99289328; PubMed=10359671;
RA Jeditlschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase."
RL Biochem. J 340:837-843(1999).
DR EMBL: AJ006054; CAB41974.1;
DR InterPro: IPR002213;
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A21F17 CRC64;

q9y4x1 length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 5 Optimized Score = 89 Significance = 0.00
Residue Identity = 19% Matches = 112 Mismatches = 336
Gaps = 117 Conservative Substitutions = 0
Translation Frame= 1

QPLQISVXGNCHEVXQVSPGISAPALLCWLMLWSPGVALXHEPLACQGHSHRAHSEKXGNSIDSL-
10 20 30 40 50 60 70
MNLNLFSLQI--SLIGTTIGNVLIWPMESG---HMLNWKIITIDELI
KAFVN---XLOEAFCEIEXGPRAT-----GQNRKKXNXCPSSECLALINLAISYKIKKXFCXNKR
80 90 100 110 120 130
KKEHNVTVLVAASGALFTTPSPNSPISLFEIYKVPFGKERIEGVKIDFVS---TWLENNPSTTWMRYQEMAK
50 60 70 80 90 100 110
NFKNDVXELYLQSDAYEEATGNG-----LRCNATRPDGS-LMRPDG-XVA---CSPPCATITXNFCRQYAK
140 150 160 170 180 190
VIRDFHWVSOEIDC--GVLRNOOLMAKLKSKFEVLVSDVPFGGDIWKLGIPE---MYSLRFSFA-
120 130 140 150 160 170
LMETSSFTLCAYDRTNRONDLSGSKKFNAPFVPLDSDL--RLSFLGR-VLXGIRKHAHYIMXDCGK
200 210 220 230 240 250 260
-----STVERKHC-----GK--VPPSPYPAVLSELTQDMSFTDRIRNEISYHLDYDFETLWK
180 190 200 210 220
SXDMANNTIIGFYXISSTIPTXLYVCMALXATCQSF-----AKGNGKFCPEF--RGRW
270 280 290 300 310
SMDSYSKALGRPTTLCETMGKAEIWLIRTYWDFEPRPYLPNEFEVGLGCKPAKPLPREMEEFIOSSGKN

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Release 5.4

Results file 09-784340-1-q9y4x1.res made by jdelaval on Sun 2 Sep 101 10:48:29-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : q9y4x1.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
Q -
U -
T -
E -
N -
C -
E -
S 0-
SCORE 0 1 2 3 4 5 6 7
STDEV

PARAMETERS

Similarity matrix Unitary K-tuple 2
Translation Frame 6
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 7 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 527
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Frame
1. q9y4x1	UDP GLUCURONOSYLTRANSFERASE (527	7	81 0.00 3

1. US-09-784-340-1 (1-2759)
q9y4x1 UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4x1 check: 7657 from: 1 to: 527

ID 09Y4X1 PRELIMINARY: PRT: 527 AA.
AC 09Y4X1:
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFACTORY;
RX MEDLINE=9289328; PubMed=10359671;
RA Jeditichky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.:
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase.";
RL Biochem. J 340:837-843(1999).
DR EMBL; AJ006054; CAB41974.1;
DR InterPro; IPR002213;
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A21F17 CRC64;

q9y4x1 Length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 7 Optimized Score = 81 Significance = 0.00
Residue Identity = 18% Matches = 108 Mismatches = 377
Gaps = 109 Conservative Substitutions = 0
Translation Frame= 3

TIADQVRELPSXGLTSLMIFCSCSSSVLAVDSVSKMCGPVYTAIGLMSRFYKSSXXEAMRXOXYLTOS
80 90 100 110 120 130 140
LRKLTGSLHLNKLKMSICHRTEQKKMYLTLXLMSCQAYOPGNLXNMTFLKXELKXKCVBALSTIR
150 160 170 180 190 200 X 210
RLKRSYRKPTTMXCLXTLPVETXWLSCLOSILCSHLEFLKALMSEAVGNFQLHPMYLCLXODXOTEXP
MLNML-----
X

220 230 240 250 260 270 280
FWKEXKIQCFQPCSTSGFRITTTIFPKGSFIVRHXEGPLHYRLMEKLRYGXEHGILNLFNHTMLTUS--L
-----LFLSLQISLIGTLGGLVLI-WPMEG---SHMLNVR--IIIDELI--KKEHVTVLVASGAL
10 20 30 40 50
290 300 310 320 330 340
LEDCTVVLKPLCLKRWK---ILSRVQSKWLVCFMGHCHFKMLQKRLSLILO-----PLPRSHRRCYG
FIFPTSN-PSLITETIYKVPQKKEIKG--VIRKPVSTWLENRSPSTIMPFYQEMAKVIRKDFHVSQELICDG
60 70 80 90 100 110 120
350 360 370 380 390 400 410
GTR-----EKNHPRHKEPILGCMIGYP--RMIFLIVIPKPLSLIMVEXGSMKLTGSGSLMWERFY--LVISL

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VLKNOQIMAKLKSFEVLVSDPVPCGDIVALKLGIPEMYSL-RFSPASTVEKHGKVPYPSYVPAVLSE
130 140 150 160 170 180 190
IT---XLTFRREOLKKTSTKLQAKIYXGL--XEOSLPILIKR--MLXDYOETMINL--XSPXIEQSSG
LTDMSFDR---IRNFISYHLDYMEFTLMSWDSYSKALGPTTLCFTMGCAEIMLIRTWDFEFPBP
200 210 220 230 240 250 260
480 490 500 510 520 530 540
SSLSGATKEPSTC---DQLP--WTPSSSTLXMXLGSCKPVMOLLVSCSONVEFPVKNLKLRKRGNR
YLPNFEFGHCHCKPAKLPKPEMEEFIOS-----SGKNGVVVSIGS-----MKNLTEKANLIASA
270 280 290 300 310 320
550 560 570 580 590 600
SFQI-QEPPDVIILLIPATXNLVKTLLF-----STYLFYILAIKPRIPKSGCEYISFRCITLGLVTLF
LAQIPQKVLKRYKGRKRPAT-LGNTQLEFDMIPONDIGHPKTKAFITHGNGIYEAI-YHGVPWGVPMFA
330 340 350 360 370 380 390
610 620 630 640 650 660 670
SHEVTOGHEVYIXIFLELISLPKXRYESNLKXGDLQYADSMCLHKHMDVKKXKXNSQNSVNHQNXSLX
DQPDNIAMKAKGAVEYNL-----NTWTSVDLLSA---LRTVINEPSYKENAMRLSRHHQPVKPL
400 410 420 430 440 450
680 690 700 710 720 730 740 750
HXLVNSNIMITFLFOFKALLHTOHXSQTMNCXKXKXGITLRIYCYISTYILXMSXPTFLPSLNKHFLCVID
DRAV--FWIEFVMRHKGAKHLRVAAHDLTWFOYHSLDIVIGFLVC--VTTAIFLVIQCCFLSCOFKRGK
460 470 480 490 500 510 520
X 760 770 780 790 800 810 820
DKXYVLIVLAKXKKLKEFSIEKMSIRTSKTDYFEISNHKKYIVISDFIKFLIVHLIXMSILXNDEYSX
KKRE
X
830 840 850 860 870 880 890
FLSLXSKYXFTVEKKRDACSESKKKKKKNTWMLPLRSVSLTAHCAVTVHYIDSDTVMLPLRSVSLTALSCVVS
900 910
VSLFALSCRYAVYKXQONTVSRYVA

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-q9y4xl.res made by jdelaval on Sun 2 Sep 101 10:48:38-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : q9y4xl.pep

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100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
E 5-
O -
U -
E -
N -
C -
E -
S 0-
SCORE 0 1 1 2 3 3 4 5 5 6
STDEV

```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Translation frame	6		
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	6	0	0.00
Times:	CPU		
	00:00:00.00		
Number of residues:	527		
Number of sequences searched:	1		
Number of scores above cutoff:	1		
		Total Elapsed	
		00:00:00.00	

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
1. q9y4xl	UDP GLUCURONOSYLTRANSFERASE (527	6	89	0.00	4

1. US-09-784-340-1 (1-2759)
q9y4xl UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4xl check: 7657 from: 1 to: 527

TOIG of: q9y4xl check: 7657 from: 1 to: 527

AC 09y4xl PRELIMINARY; PRT; 527 AA.

DT 01-NOV-1999 (Tremblrel. 12. Created)

DT 01-NOV-1999 (Tremblrel. 12. Last sequence update)

DT 01-MAY-2000 (Tremblrel. 13. Last annotation update)

DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

GN UGT2A1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=OLFATORY;

RX MEDLINE=9289328; PubMed=10359671;

RA "Jedlitschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;

RT "Cloning and characterization of a novel human olfactory UDP-

RT glucuronosyltransferase.";

RL Biochem. J 340:837-843(1999).

DR EMBL; AJ006054; CAB41974.1; .

DR InterPro; IPR002213; .

DR Pfam; PF00201; UDPGT; 1.

DR PROSITE; PS00375; UDPGT; 1.

KW Transferase; Glycosyltransferase.

SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A421F17 CRC64;

09y4xl length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 6 Optimized Score = 89 Significance = 0.00

Residue Identity = 20% Matches = 119 Mismatches = 360

Gaps = 116 Conservative Substitutions = 0

Translation Frame= 4

RYVTADSVLLSTIRYVTAQXCCORVARNAXQCCORVATXRHDSVAVNDMLNGMTVGCORVATXRHDSVFEF

80 90 100 110 120 130 140

FFFTFRSISLFEYSKLYFLKXREKLVFLIKNRHNOVYQOLKFKIRNYNHIFLMTYLLKIIICLTIXISY

150 160 170 180 190 200 210

GHLFVVRKFOFLLEFDNNKNCLEFLIKNTQKMSYKWKQCKRLHLDVCGNIAMISCNALSSFLAHCLRS

220 230 240 250 260 270 280

VMLGKXKGLFLKKNHVTNKLMSKNASLICYVYXILKILHFLLYIHVFTPGISILQVTL--SLKVR

290 300 310 320 330 340 350

EVMT-----SMKQYQKXENLDVFWSLCHKVRRESKHTXENATREXDLITTSXSMNSRLYSXDKITEYLK

360 370 380 390 400

LIGTLGNGVLIWPEGSHMLNVKLIIDELIKKEHNVTVLVASGALFTPTPS--NPSL-----TFEIKYV

410 420 430 440 450

XOGFHOILCGMNXYPIRSF--LNLK--RSIPSFLSFXFY-----XIFDKIKINILKTRIXO

460 470 480 490 500

PRGKERI-----EGVAKDFSTVLENRPSPS--TIWRFYQEMAKVICKDFHNVSOELCDGVILKN-----OO

510 520 530 540 550

80 90 100 110 120 130

410 420 430 440 450 460 470

LPHRSAGTQSHLSAGATRXGHGQILAGANLQGANQOTSRRLDDGALQVHGGEFLIISXSLYKRNRRXL

480 490 500 510 520 530 540

LMKILKSKFEVLVS--DPVPCGDIVA--LKLGIPEWYS--LRSPASTVEKKCKGVPPSYVAVAVSEL

550 560 570 580 590 600

FSKPSVNLRLSKFXSLFLQ-----LLIMPSCELCY-QADHQIMEL-PPXGPHGKXLR-SHSFHHKXKLMFW

610 620 630 640 650 660 670

TDQMSFTDRIKNEISYHLDQVMEFTLMSKMSDYSKALGRPTLLCETMGAEIWLIRTYWDFEFPRLY---

680 690 700 710 720 730 740

DDQDHDHGVSNHTREYVLLMMVPELCTSIPTSVSGGGLKQXIXPFLAHFEVTPER-----TPQ

750 760 770 780 790 800 810

PNFEFVGLHCKPA-KPLPKMEEF-----IQSSGKNG-----VVFESIGSMVKNLIEKANKLIASALAIPO

820 830 840 850 860 870 880

YHLELNSGQNPFPFXAKMLQVYSALLO---QTSXGVGMVEIIONPMEVLAISQLFPOSHIMXWALMPYK

890 900 910 920 930 940 950

KVLMRYKG-KKPAITLGNNTOLFDMITPONDLIGHPKTKAFITHGFTNGIYEAHYHGVF-----MVGVPWFA

960 970 980 990 1000

TLPKNDSNPESRSQTKLALNLFLLFPERSCFLVLSXAOYHRRVLELVSHSPAYCLLOKFXVXQKGL-Q

1010 1020 1030 1040 1050 1060 1070

DOFNN-----IAHKAKGAAYEVNLTMTSYDL-----SALRTVINPEPSYKENAMRLSRITHNDQPVKPLDR

1080 1090 1100 1110 1120 1130 1140

ATQPSGLHRESQGLALHRSWEPVASSYASDCRASSHTS--FLKFLFQOKNHILKILARLISLARHSELG

1150 1160 1170 1180 1190 1200

AVFWLEFVWRHKG--AKH--LRVA---AHDLTWFQYHSLDVIGFLVCVTTAIFLVIQCCFLFCQKFGKIG

1210 1220 1230 1240 1250 1260 1270

820 X 830 840 850 860 870 880

QQIFHFLFCEPVAAYGPPDISMOKASCQSQTALSESILLPHGLSLXALLEKXPXKXANGSCHRAATPGLSHRTH

890 900 910 920 930 940 950

SOHRRRAGAEIPLKLCQISXWQFPHTLIGN

960 970 980 990 1000

KKKKRE

890 900 910 920 930 940 950

SOHRRRAGAEIPLKLCQISXWQFPHTLIGN


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VSDPFFPGDIIVALKLGIPIFWYSLRFPSPASTVEKHKGVPPSPYVPAVLSELDJMSFTDRINFTSYH--
150      160      170      180      190      200      210
420      430      440      450      460      470
OQEPNHIYRVVLEPGEVNGSKXSQVIG-----SEVAHDKL-----DPECCSTXGLYRLIMVNSXXSHSL
-----LQDVWFETLMKSMPSYSKALGRPTTLCETMGKAEIMLIRTYWDFE-----FPRPLPN-----
220      230      240      250      260      270
480      490      500      510      520      530
ETRGIGNDOSQSPQXIFRCHSEFVYFYSCSEGLHY-----SVYIKLITKYNSHHDPVNVNFEIDPIHSTMSD
ETRGIGNDOSQSPQXIFRCHSEFVYFYSCSEGLHY-----SVYIKLITKYNSHHDPVNVNFEIDPIHSTMSD
280      290      300      310      320      330
FEFVGGLHC--RPAKPLREMEFIOSSGKNGVVFSGSWKNTLTERKAN-----LIASALAOI-----PO
540      550      560      570      580      590
KSPGFGWTK-----ILSGYPIITQPSIGSKGWFSPFPVPHXLMIDLGKXSNDISLEFC
KSPGFGWTK-----ILSGYPIITQPSIGSKGWFSPFPVPHXLMIDLGKXSNDISLEFC
340      350      360      370      380      390
KVLNRYKGRKPAITLGNNTOLFPMIPQNDLLGHPKTKAFL--THGTINGIYEALYHGVPMVGVPMFAD---QPD
600      610      620      630      640
NT-----LKQXPOKHHNTTFFPYTLDKIFHFLRQSEFGRFVY--QSSNK--LKVRL-----VWLKKEKIP
NT-----LKQXPOKHHNTTFFPYTLDKIFHFLRQSEFGRFVY--QSSNK--LKVRL-----VWLKKEKIP
400      410      420      430      440      450      460
NIAHMKAKGAAYEVNLT---MISVDLSALR-----TVINEPSYKENAMRLSRHHDPVKKPLDRAVEWI
NIAHMKAKGAAYEVNLT---MISVDLSALR-----TVINEPSYKENAMRLSRHHDPVKKPLDRAVEWI
650      660      670      680      690      700      710      720
CSYXPLYLSFHSILTXCSGSPXCLTIKLFPMIYVILNPEEONKXKHIFYSFGKSHVCSXCHRRHYTGKWS
CSYXPLYLSFHSILTXCSGSPXCLTIKLFPMIYVILNPEEONKXKHIFYSFGKSHVCSXCHRRHYTGKWS
470      480      490      500      510      520
EFVRRHKGAKH---LRVAHDLT-WFOYHSLDIVIGELLY--CVTAIFLVIO---CCLFSCOKFGKIGK--
EFVRRHKGAKH---LRVAHDLT-WFOYHSLDIVIGELLY--CVTAIFLVIO---CCLFSCOKFGKIGK--
730      740      750      760      770      780      790
WKFPYASLHIASTRNSKCEHRRDCKQLSHQVSTGNHRVYKHYYIVGFLXLLHKLRLIYDKALTLHFFXSSSYFN
WKFPYASLHIASTRNSKCEHRRDCKQLSHQVSTGNHRVYKHYYIVGFLXLLHKLRLIYDKALTLHFFXSSSYFN
-----KKKRE
800      810      820      830      840      850      860
KILIXFYNLPGXXAMODIOSXVNRKYPIFFCSVLMHMDHLKFOCRRLPYVNXKRLXYSQCYIMASHYELFX
KILIXFYNLPGXXAMODIOSXVNRKYPIFFCSVLMHMDHLKFOCRRLPYVNXKRLXYSQCYIMASHYELFX
870      880      890      900      910
NDLDIKYMAHVTGPHDPPTTESTANTELEOKYOSXLVPRHDGSSLTHXSAM
NDLDIKYMAHVTGPHDPPTTESTANTELEOKYOSXLVPRHDGSSLTHXSAM

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

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Results file 09-784340-1-q9y4xl.res made by jdelaval on Sun 2 Sep 101 10:48:53-PDT.

```

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

```

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Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : q9y4xl.pep

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100-
N -
U - 50-
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F - 10-
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E - 5-
Q -
U -
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E -
S - 0-
SCORE 0 1 1 2 3 3 4 5 5 6
STDEV

```

PARAMETERS

```

Similarity matrix      Unitary      K-tuple      2
Translation Frame      6
Mismatch penalty      1.00      Joining penalty      20
Gap size penalty      0.05      Window size      32
Cutoff score          1
Randomization group    0

```

SEARCH STATISTICS

```

Scores:      Mean      Median      Standard Deviation
5            0            0.00

Times:      CPU      Total Elapsed
00:00:00.00      527      00:00:00.00
Number of residues: 527
Number of sequences searched: 1
Number of scores above cutoff: 1

```

The scores below are sorted by initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Frame
1. q9y4xl	UDP GLUCURONOSYLTRANSFERASE (527	6	83 0.00 6

1. US-09-784-340-1 (1-2759)
q9y4xl UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4xl check: 7657 from: 1 to: 527

ID Q9Y4XL PRELIMINARY; PRT; 527 AA.
AC Q9Y4XL;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFATORY;
RX MEDLINE=99289328; PubMed=10359671;
RA Uedlitschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase."
RL Biochem. J 340:837-843(1999).
DR EMBL: AJ006054; CAB41974.1; .
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DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A421F17 CRC64;

Q9Y4XL Length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 6 Optimized Score = 83 Significance = 0.00
Residue Identity = 19% Matches = 116 Mismatches = 333
Gaps = 150 Conservative Substitutions = 0
Translation Frame= 6

LRNGXQCFRAVNDTLRNGMTVLSTIRSKRMVLTSTIRVTAQCRCQRYATXRHDSGLSTIRVTAQCFFEF
80 90 100 110 120 130 140
FFYQNKRLFLLQXIIILLIIEIRIMSIHFKREKTFKSSVLSIKILXNQKLOSHSNGYLSQNNLNLILM
MLNLL
X

150 160 170 180 190 200 210
TFSLCKRTSVSFIIXGXQXELSIYHOEFTKRVSNYMAEMXAMTSKXGMKYS-KLFXVXCPVIFVSN-SL-S
LFSL-QISLIGTLGCVNLWIPMEGSHWLVNKIIIDELIKKEHNVTLVASGALF-----TTPTSNPSLTF
10 20 30 40 50 60 70

220 230 240 250 260 270
ET-----SNAGVEGLI-----XTEKES-----LCYSQXANVIECFIDGLNLFVFTFTSLHPVCAN
EIVYVPCKRIEGLVTKDFVSTWLENRPSTIMRFYQEMAKVTKDF-----HMSOEICDGYL
80 90 100 110 120 130

280 290 300 310 320
TRNQHGHPTTXGRSNDVMEVISELGRFC--IHYL-----VSOSERREXA-----HLGKCNEMRY--
KNQOLMA-----KLKSKFEVLVS-DVFPCCGDIYALKLGIIPMYSLRSFSPASTVEKHCGKVPYPPSYVP
140 150 160 170 180 190

330 340 350 360 370 380 390
--THNLMIMEFFXALIXLRXNRI-----DNM-KIARESPNMMELTGLPHQVPLEEGKITSLFSLVLLN
AVSELDDQMSF---TRIRNFISYHODVYEFELMKSMDSYSKALGRPTTLCETGK-----AEIWLIRFY
200 210 220 230 240 250
400 410 420 430 440 450
FXQENKHFVFNKNIATVATQVSRNPITSIEXCQNVQVRSWADNRCLAPL-WMTNLSIO---KTARSRGFTGXS
WDPE-----FPRPLPNEFVPGHCKPA-----KLPRKMEEFIOSSGNGVVSIGSM
260 270 280 290 300 310
460 470 480 490 500 510
WXIL-----DNLIAFSL--XEEVMTVLKALSKSL-----VIYLFISTAPLAFMXAMLSXSP
VKNLTEKANIILASALQIPQKVLMMRKKGKRPATLGNTOLEFDWIPONDLLGHKTAFITHGNTGNIYAI
320 330 340 350 360 370 380
520 530 540 550 560 570 580
NMGPTIGTPMXIASXIPFIPPYVYK-ALVYLGXPRRSFGIOSYRVLPAPVNDGFFPLYLHNTFCGIARAE
YHGVPMYGVF-MFADQPDNITAMAKGAAY-----EVNLNTFTSYDLSALPTVINEBSYKEN-----
390 400 410 420 430
590 600 610 620 630 640
AMIL-----AFSSVTFXNSDPRENTTIPSPELMTKFSISLGLKALAGLCQCNPTNSKLGWGX
AMRSLRIHHQPVKPLDRAVWVIEFVNRHKGAKHLRVAAHDLTFQYHSLDVLGFLVC-VTFALFVLVIGCC
440 450 460 470 480 490 500 510
650 660 670 680 690 700 710
GNSKQYVRISHISAFPTVSHNVVGLPNNALLNNSQXXSXIXIQKWNKTESIEFFTLRSKVLVSVPVIGT
LFSQCKRGKIGKKKRE
520 X
720 730 740 750 760 770 780
GTXSAGSGFPQLRSILPPTIELSVSTKGTASNSAIRSPQGITGSISITSXLYVSCSPFISVXLKIKLSHILF
790 800 810 820 830 840 850
KVPILSTKKSFPNFTTDCQVDRPGKTFPARRSTINISFSSVLSGCIWTTTSNFMNGLXISNEGFEAVNVTWSP
860 870 880 890 900 910
LTMSSSRMTLTLISQMLMSQGHTRFPQNPQPTOKSCRSRNTKADLSLDMMAVPSHTDLOW

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